

## SEQUENCE SUBMISSION

SEQ ID NO: 1 provides rodent IL-1 $\delta$  nucleotide sequence.  
SEQ ID NO: 2 provides rodent IL-1 $\delta$  polypeptide sequence.  
5 SEQ ID NO: 3 provides partial rodent IL-1 $\epsilon$  nucleotide sequence.  
SEQ ID NO: 4 provides partial rodent IL-1 $\epsilon$  polypeptide sequence.  
SEQ ID NO: 5 provides full length rodent IL-1 $\epsilon$  nucleic acid sequence.  
SEQ ID NO: 6 provides full length rodent IL-1 $\epsilon$  polypeptide sequence.  
SEQ ID NO: 7 provides human IL-1RA precursor polypeptide sequence.  
10 SEQ ID NO: 8 provides human IL-1 $\gamma$  (IGIF) precursor polypeptide sequence.  
SEQ ID NO: 9 provides mouse IL-1 $\gamma$  (IGIF) precursor polypeptide sequence.  
SEQ ID NO: 10 provides human IL-1 $\beta$  precursor polypeptide sequence.  
SEQ ID NO: 11 provides human IL-1 $\alpha$  precursor polypeptide sequence.  
SEQ ID NO: 12 provides primate IL-1 $\epsilon$  nucleotide sequence.  
15 SEQ ID NO: 13 provides primate IL-1 $\epsilon$  polypeptide sequence.  
SEQ ID NO: 14 provides full length primate IL-1 $\epsilon$  nucleic acid sequence.  
SEQ ID NO: 15 provides full length primate IL-1 $\epsilon$  polypeptide sequence.

## 20 (1) GENERAL INFORMATION:

(i) APPLICANT: Hedrick, Joseph A.  
Sana, Theodore R.  
25 Bazan, Fernando J.  
Kastelein, Robert A.

(ii) TITLE OF INVENTION: Mammalian Cytokines; Related Reagents  
and Methods

30 (iii) NUMBER OF SEQUENCES: 15

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## 40 (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
45 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US  
(B) FILING DATE: 07-AUG-1998  
50 (C) CLASSIFICATION:

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/044,165  
(B) FILING DATE: 21-APR-1997

## 55 (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/055,111  
(B) FILING DATE: 06-AUG-1997

## 60 (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 09/062,866

(B) FILING DATE: 20-APR-1998

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 09/097,976

(B) FILING DATE: 16-JUN-1998

## (viii) ATTORNEY/AGENT INFORMATION:

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## (ix) TELECOMMUNICATION INFORMATION:

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## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 470 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..468

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

35	ATG ATG GTT CTG AGT GGG GCA CTA TGC TTC CGA ATG AAG GAT TCA GCC	48
	Met Met Val Leu Ser Gly Ala Leu Cys Phe Arg Met Lys Asp Ser Ala	
	1 5 10 15	
40	TTG AAG GTA CTG TAT CTG CAC AAT AAC CAG CTG CTG GCT GGA GGA CTG	96
	Leu Lys Val Leu Tyr Leu His Asn Asn Gln Leu Leu Ala Gly Gly Leu	
	20 25 30	
45	CAC GCA GAG AAG GTC ATT AAA GGT GAG GAG ATC AGT GTT GTC CCA AAT	144
	His Ala Glu Lys Val Ile Lys Gly Glu Glu Ile Ser Val Val Pro Asn	
	35 40 45	
50	CGG GCA CTG GAT GCC AGT CTG TCC CCT GTC ATC CTG GGC GTT CAA GGA	192
	Arg Ala Leu Asp Ala Ser Leu Ser Pro Val Ile Leu Gly Val Gln Gly	
	50 55 60	
55	GGA AGC CAG TGC CTA TCT TGT GGG ACA GAG AAA GGG CCA ATT CTG AAA	240
	Gly Ser Gln Cys Leu Ser Cys Gly Thr Glu Lys Gly Pro Ile Leu Lys	
	65 70 75 80	
60	CTT GAG CCA GTG AAC ATC ATG GAG CTC TAC CTC GGG GCC AAG GAA TCA	288
	Leu Glu Pro Val Asn Ile Met Glu Leu Tyr Leu Gly Ala Lys Glu Ser	
	85 90 95	
60	AAG AGC TTC ACC TTC TAC CGG CGG GAT ATG GGT CTT ACC TCC AGC TTC	336
	Lys Ser Phe Thr Phe Tyr Arg Arg Asp Met Gly Leu Thr Ser Ser Phe	

	100	105	110		
5	GAA TCC GCT GCC TAC CCA GGC TGG TTC CTC TGC ACC TCA CCG GAA GCT Glu Ser Ala Ala Tyr Pro Gly Trp Phe Leu Cys Thr Ser Pro Glu Ala	115	120	125	384
10	GAC CAG CCT GTC AGG CTC ACT CAG ATC CCT GAG GAC CCC GCC TGG GAT Asp Gln Pro Val Arg Leu Thr Gln Ile Pro Glu Asp Pro Ala Trp Asp	130	135	140	432
15	GCT CCC ATC ACA GAC TTC TAC TTT CAG CAG TGT GAC TA Ala Pro Ile Thr Asp Phe Tyr Phe Gln Gln Cys Asp	145	150	155	470

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Met	Val	Leu	Ser	Gly	Ala	Leu	Cys	Phe	Arg	Met	Lys	Asp	Ser	Ala	1	5	10	15
Leu	Lys	Val	Leu	Tyr	Leu	His	Asn	Asn	Gln	Leu	Leu	Ala	Gly	Gly	Leu	20	25	30	
His	Ala	Glu	Lys	Val	Ile	Lys	Gly	Glu	Glu	Ile	Ser	Val	Val	Pro	Asn	35	40	45	
Arg	Ala	Leu	Asp	Ala	Ser	Leu	Ser	Pro	Val	Ile	Leu	Gly	Val	Gln	Gly	50	55	60	
Gly	Ser	Gln	Cys	Leu	Ser	Cys	Gly	Thr	Glu	Lys	Gly	Pro	Ile	Leu	Lys	65	70	75	80
Leu	Glu	Pro	Val	Asn	Ile	Met	Glu	Leu	Tyr	Leu	Gly	Ala	Lys	Glu	Ser	85	90	95	
Lys	Ser	Phe	Thr	Phe	Tyr	Arg	Arg	Asp	Met	Gly	Leu	Thr	Ser	Ser	Phe	100	105	110	
Glu	Ser	Ala	Ala	Tyr	Pro	Gly	Trp	Phe	Leu	Cys	Thr	Ser	Pro	Glu	Ala	115	120	125	
Asp	Gln	Pro	Val	Arg	Leu	Thr	Gln	Ile	Pro	Glu	Asp	Pro	Ala	Trp	Asp	130	135	140	
Ala	Pro	Ile	Thr	Asp	Phe	Tyr	Phe	Gln	Gln	Cys	Asp					145	150	155	

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs

5 (ii) MOLECULE TYPE: cDNA

10 (A) NAME/KEY: CDS  
(B) LOCATION: 1..216

15    TTC CAG GAA GGG AAC ATA ATG GAA ATG TAC AAC AAA AAG GAA CCT GTA                  48  
     Phe Gln Glu Gly Asn Ile Met Glu Met Tyr Asn Lys Lys Glu Pro Val  
           1                              5                                      10    15

AAA GCC TCT CTC TTC TAT CAC AAG AAG AGT GGT ACA ACC TCT ACA TTT  
Lys Ala Ser Leu Phe Tyr His Lys Lys Ser Gly Thr Thr Ser Thr Phe

20                  25                  30

96

25 GAG TCT GCA GCC TTC CCT GGT TGG TTC ATC GCT GTC TGC TCT AAA GGG 144  
Glu Ser Ala Ala Phe Pro Gly Trp Phe Ile Ala Val Cys Ser Lys Gly  
35 40 45

AGC TGC CCA CTC ATT CTG ACC CAA GAA CTG GGG GAA ATC TTC ATC ACT 192  
Ser Cys Pro Leu Ile Leu Thr Gln Glu Leu Gly Glu Ile Phe Ile Thr  
50 55 60

GAC TTC GAG ATG ATT GTG GTA CAT TAA  
Asp Phe Glu Met Ile Val Val His  
65 70

35 (2) INFORMATION FOR SEQ ID NO:4:

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 72 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Phe Gln Glu Gly Asn Ile Met Glu Met Tyr Asn Lys Lys Glu Pro Val  
1 5 10 15

50    Lys Ala Ser Leu Phe Tyr His Lys Lys Ser Gly Thr Thr Ser Thr Phe  
                        20                        25                        30

Glu Ser Ala Ala Phe Pro Gly Trp Phe Ile Ala Val Cys Ser Lys Gly  
35 40 45

Ser Cys Pro Leu Ile Leu Thr Gln Glu Leu Gly Glu Ile Phe Ile Thr  
50 55 60

60      Asp Phe Glu Met Ile Val Val His  
          65                          70

## (2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 809 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 90..569

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

20	GAATTCGGCA CGAGTGTAGT GTGCAGACAC ATTCCTTATT CAATCAGGGT CAATCTGCAG	60
	ATTGGCAGCT CAGGAACAAC ATCACCATA ATG AAT AAG GAG AAA GAA CTA AGA	113
	Met Asn Lys Glu Lys Glu Leu Arg	
	1 5	
25	GCA GCA TCA CCT TCG CTT AGA CAT GTT CAG GAT CTT AGT AGT CGT GTG	161
	Ala Ala Ser Pro Ser Leu Arg His Val Gln Asp Leu Ser Ser Arg Val	
	10 15 20	
30	TGG ATC CTG CAG AAC AAT ATC CTC ACT GCA GTC CCA AGG AAA GAG CAA	209
	Trp Ile Leu Gln Asn Asn Ile Leu Thr Ala Val Pro Arg Lys Glu Gln	
	25 30 35 40	
35	ACA GTT CCA GTC ACT ATT ACC TTG CTC CCA TGC CAA TAT CTG GAC ACT	257
	Thr Val Pro Val Thr Ile Thr Leu Leu Pro Cys Gln Tyr Leu Asp Thr	
	45 50 55	
	CTT GAG ACG AAC AGG GGG GAT CCC ACG TAC ATG GGA GTG CAA AGG CCG	305
40	Leu Glu Thr Asn Arg Gly Asp Pro Thr Tyr Met Gly Val Gln Arg Pro	
	60 65 70	
	ATG AGC TGC CTG TTC TGC ACA AAG GAT GGG GAG CAG CCT GTG CTA CAG	353
	Met Ser Cys Leu Phe Cys Thr Lys Asp Gly Glu Gln Pro Val Leu Gln	
	75 80 85	
45	CTT GGG GAA GGG AAC ATA ATG GAA ATG TAC AAC AAA AAG GAA CCT GTA	401
	Leu Gly Glu Gly Asn Ile Met Glu Met Tyr Asn Lys Lys Glu Pro Val	
	90 95 100	
50	AAA GCC TCT CTC TTC TAT CAC AAG AAG AGT GGT ACA ACC TCT ACA TTT	449
	Lys Ala Ser Leu Phe Tyr His Lys Lys Ser Gly Thr Thr Ser Thr Phe	
	105 110 115 120	
55	GAG TCT GCA GCC TTC CCT GGT TGG TTC ATC GCT GTC TGC TCT AAA GGG	497
	Glu Ser Ala Ala Phe Pro Gly Trp Phe Ile Ala Val Cys Ser Lys Gly	
	125 130 135	
	AGC TGC CCA CTC ATT CTG ACC CAA GAA CTG GGG GAA ATC TTC ATC ACT	545
60	Ser Cys Pro Leu Ile Leu Thr Gln Glu Leu Gly Glu Ile Phe Ile Thr	
	140 145 150	

GAC TTC GAG ATG ATT GTG GTA CAT TAAGGTTTTT AGACACATTG CTCTGTGGCA 599  
 Asp Phe Glu Met Ile Val Val His  
 155 160  
 5 CTCTCTCAAG ATTTCTTGGA TTCTAACAAG AAGCAATCAA AGACACCCCT AACAAAATGG 659  
 AAGACTGAAA AGAAAGCTGA GCCCTCCCTG GGCTGTTTTT CCTTGGTGGT GAATCAGATG 719  
 10 CAGAACATCT TACCATGTTT TCATCCAAAG CATTTACTGT TGGTTTTTAC AAGGAGTGAA 779  
 TTTTTTAAAA TAAAATCATT TATCTCATAA 809

15 (2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids  
 (B) TYPE: amino acid  
 20 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

25 Met Asn Lys Glu Lys Glu Leu Arg Ala Ala Ser Pro Ser Leu Arg His  
 1 5 10 15  
 30 Val Gln Asp Leu Ser Ser Arg Val Trp Ile Leu Gln Asn Asn Ile Leu  
 20 25 30  
 Thr Ala Val Pro Arg Lys Glu Gln Thr Val Pro Val Thr Ile Thr Leu  
 35 35 40 45  
 Leu Pro Cys Gln Tyr Leu Asp Thr Leu Glu Thr Asn Arg Gly Asp Pro  
 50 55 60  
 40 Thr Tyr Met Gly Val Gln Arg Pro Met Ser Cys Leu Phe Cys Thr Lys  
 65 70 75 80  
 Asp Gly Glu Gln Pro Val Leu Gln Leu Gly Glu Gly Asn Ile Met Glu  
 85 90 95  
 45 Met Tyr Asn Lys Lys Glu Pro Val Lys Ala Ser Leu Phe Tyr His Lys  
 100 105 110  
 Lys Ser Gly Thr Thr Ser Thr Phe Glu Ser Ala Ala Phe Pro Gly Trp  
 115 120 125  
 50 Phe Ile Ala Val Cys Ser Lys Gly Ser Cys Pro Leu Ile Leu Thr Gln  
 130 135 140  
 Glu Leu Gly Glu Ile Phe Ile Thr Asp Phe Glu Met Ile Val Val His  
 145 150 155 160  
 55

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 177 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: peptide

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Glu Ile Cys Arg Gly Leu Arg Ser His Leu Ile Thr Leu Leu Leu  
1 5 10 15  
Phe Leu Phe His Ser Glu Thr Ile Cys Arg Pro Ser Gly Arg Lys Ser  
20 25 30  
Ser Lys Met Gln Ala Phe Arg Ile Trp Asp Val Asn Gln Lys Thr Phe  
35 40 45  
Tyr Leu Arg Asn Asn Gln Leu Val Ala Gly Tyr Leu Gln Gly Pro Asn  
50 55 60  
Val Asn Leu Glu Glu Lys Ile Asp Val Val Pro Ile Glu Pro His Ala  
65 70 75 80  
Leu Phe Leu Gly Ile His Gly Gly Lys Met Cys Leu Ser Cys Val Lys  
85 90 95  
Ser Gly Asp Glu Thr Arg Leu Gln Leu Glu Ala Val Asn Ile Thr Asp  
100 105 110  
Leu Ser Glu Asn Arg Lys Gln Asp Lys Arg Phe Ala Phe Ile Arg Ser  
115 120 125  
Asp Ser Gly Pro Thr Thr Ser Phe Glu Ser Ala Ala Cys Pro Gly Trp  
130 135 140  
Phe Leu Cys Thr Ala Met Glu Ala Asp Gln Pro Val Ser Leu Thr Asn  
145 150 155 160  
Met Pro Asp Glu Gly Val Met Val Thr Lys Phe Tyr Phe Gln Glu Asp  
165 170 175  
45 Glu

(2) INFORMATION FOR SEQ ID NO:8:

50 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 193 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: peptide

60

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

5 Met Ala Ala Glu Pro Val Glu Asp Asn Cys Ile Asn Phe Val Ala Met  
 1 5 10 15  
 Lys Phe Ile Asp Asn Thr Leu Tyr Phe Ile Ala Glu Asp Asp Glu Asn  
 20 25 30  
 10 Leu Glu Ser Asp Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile  
 35 40 45  
 Arg Asn Leu Asn Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro  
 50 55 60  
 15 Leu Phe Glu Asp Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro Arg  
 65 70 75 80  
 Thr Ile Phe Ile Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met  
 85 90 95  
 20 Ala Val Thr Ile Ser Val Lys Cys Glu Lys Ile Ser Thr Leu Ser Cys  
 100 105 110  
 Glu Asn Lys Ile Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile  
 115 120 125  
 25 Lys Asp Thr Lys Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly  
 130 135 140  
 30 His Asp Asn Lys Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr Phe  
 145 150 155 160  
 Leu Ala Cys Glu Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys  
 165 170 175  
 35 Glu Asp Glu Leu Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu  
 180 185 190  
 40 Asp

## (2) INFORMATION FOR SEQ ID NO:9:

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 192 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: not relevant  
 (D) TOPOLOGY: linear  
 50 (ii) MOLECULE TYPE: peptide

## 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

60 Met Ala Ala Met Ser Glu Asp Ser Cys Val Asn Phe Lys Glu Met Met  
 1 5 10 15  
 Phe Ile Asp Asn Thr Leu Tyr Phe Ile Pro Glu Glu Asn Gly Asp Leu



	20	25	30
5	Glu Ser Asp Asn Phe Gly Arg Leu His Cys Thr Thr Ala Val Ile Arg 35 40 45		
	Asn Ile Asn Asp Gln Val Leu Phe Val Asp Lys Arg Gln Pro Val Phe 50 55 60		
10	Glu Asp Met Thr Asp Ile Asp Gln Ser Ala Ser Glu Pro Gln Thr Arg 65 70 75 80		
	Leu Ile Ile Tyr Met Tyr Lys Asp Ser Glu Val Arg Gly Leu Ala Val 85 90 95		
15	Thr Leu Ser Val Lys Asp Ser Lys Met Ser Thr Leu Ser Cys Lys Asn 100 105 110		
	Lys Ile Ile Ser Phe Glu Glu Met Asp Pro Pro Glu Asn Ile Asp Asp 115 120 125		
20	Ile Gln Ser Asp Leu Ile Phe Phe Gln Lys Arg Val Pro Gly His Asn 130 135 140		
	Lys Met Glu Phe Glu Ser Ser Leu Tyr Glu Gly His Phe Leu Ala Cys 145 150 155 160		
25	Gln Lys Glu Asp Asp Ala Phe Lys Leu Ile Leu Lys Lys Lys Asp Glu 165 170 175		
30	Asn Gly Asp Lys Ser Val Met Phe Thr Leu Thr Asn Leu His Gln Ser 180 185 190		

## (2) INFORMATION FOR SEQ ID NO:10:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: not relevant  
 (D) TOPOLOGY: linear

40

## (ii) MOLECULE TYPE: peptide

45

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

50	Met Ala Glu Val Pro Lys Leu Ala Ser Glu Met Met Ala Tyr Tyr Ser 1 5 10 15
	Gly Asn Glu Asp Asp Leu Phe Phe Glu Ala Asp Gly Pro Lys Gln Met 20 25 30
55	Lys Cys Ser Phe Gln Asp Leu Asp Leu Cys Pro Leu Asp Gly Gly Ile 35 40 45
60	Gln Leu Arg Ile Ser Asp His His Tyr Ser Lys Gly Phe Arg Gln Ala 50 55 60

Ala Ser Val Val Val Ala Met Asp Lys Leu Arg Lys Met Leu Val Pro  
65 70 75 80

5 Cys Pro Gln Thr Phe Gln Glu Asn Asp Leu Ser Thr Phe Phe Pro Phe  
85 90 95

Ile Phe Glu Glu Glu Pro Ile Phe Phe Asp Thr Trp Asp Asn Glu Ala  
100 105 110

10 Tyr Val His Asp Ala Pro Val Arg Ser Leu Asn Cys Thr Leu Arg Asp  
115 120 125

Ser Gln Gln Lys Ser Leu Val Met Ser Gly Pro Tyr Glu Leu Lys Ala  
130 135 140

15 Leu His Leu Gln Gly Gln Asp Met Glu Gln Gln Val Val Phe Ser Met  
145 150 155 160

20 Ser Phe Val Gln Gly Glu Glu Ser Asn Asp Lys Ile Pro Val Ala Leu  
165 170 175

Gly Leu Lys Glu Lys Asn Leu Tyr Leu Ser Cys Val Leu Lys Asp Asp  
180 185 190

25 Lys Pro Thr Leu Gln Leu Glu Ser Val Asp Pro Lys Asn Tyr Pro Lys  
195 200 205

Lys Lys Met Glu Lys Arg Phe Val Phe Asn Lys Ile Glu Ile Asn Asn  
210 215 220

30 Lys Leu Glu Phe Glu Ser Ala Gln Phe Pro Asn Trp Tyr Ile Ser Thr  
225 230 235 240

35 Ser Gln Ala Glu Asn Met Pro Val Phe Leu Gly Gly Thr Lys Gly Gly  
245 250 255

Gln Asp Ile Thr Asp Phe Thr Met Gln Phe Val Ser Ser  
260 265

40 (2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids  
(B) TYPE: amino acid  
45 (C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

55 Met Ala Lys Val Pro Asp Met Phe Glu Asp Leu Lys Asn Cys Tyr Ser  
1 5 10 15

Glu Asn Glu Glu Asp Ser Ser Ser Ile Asp His Leu Ser Leu Asn Gln  
20 25 30

60

Lys Ser Phe Tyr His Val Ser Tyr Gly Pro Leu His Glu Gly Cys Met  
 35 40 45  
 5 Asp Gln Ser Val Ser Leu Ser Ile Ser Glu Thr Ser Lys Thr Ser Lys  
 50 55 60  
 Leu Thr Phe Lys Glu Ser Met Val Val Val Ala Thr Asn Gly Lys Val  
 65 70 75 80  
 10 Leu Lys Lys Arg Arg Leu Ser Leu Ser Gln Ser Ile Thr Asp Asp Asp  
 85 90 95  
 Leu Glu Ala Ile Ala Asn Asp Ser Glu Glu Glu Ile Ile Lys Pro Arg  
 100 105 110  
 15 Ser Ala Pro Phe Ser Phe Leu Ser Asn Val Lys Tyr Asn Phe Met Arg  
 115 120 125  
 Ile Ile Lys Tyr Glu Phe Ile Leu Asn Asp Ala Leu Asn Gln Ser Ile  
 130 135 140  
 Ile Arg Ala Asn Asp Gln Tyr Leu Thr Ala Ala Ala Leu His Asn Leu  
 145 150 155 160  
 25 Asp Glu Ala Val Lys Phe Asp Met Gly Ala Tyr Lys Ser Ser Lys Asp  
 165 170 175  
 Asp Ala Lys Ile Thr Val Ile Leu Arg Ile Ser Lys Thr Gln Leu Tyr  
 180 185 190  
 30 Val Thr Ala Gln Asp Glu Asp Gln Pro Val Leu Leu Lys Glu Met Pro  
 195 200 205  
 Glu Ile Pro Lys Thr Ile Thr Gly Ser Glu Thr Asn Leu Leu Phe Phe  
 210 215 220  
 Trp Glu Thr His Gly Thr Lys Asn Tyr Phe Thr Ser Val Ala His Pro  
 225 230 235 240  
 40 Asn Leu Phe Ile Ala Thr Lys Gln Asp Tyr Trp Val Cys Leu Ala Gly  
 245 250 255  
 Gly Pro Pro Ser Ile Thr Asp Phe Gln Ile Leu Glu Asn Gln Ala  
 260 265 270  
 45

## (2) INFORMATION FOR SEQ ID NO:12:

## (i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 505 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

55

## (ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 1..504  
 60

007096-02502200

## (ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 144

5 (D) OTHER INFORMATION: /note= "nucleotide 144 designated  
G, may be G or T"

## (ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 451

10 (D) OTHER INFORMATION: /note= "nucleotide 451 designated  
C, may be C or T"

## (ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 469

15 (D) OTHER INFORMATION: /note= "nucleotide 469 designated  
C, may be A, C, G, or T"

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATG AGA GGC ACT CCA GGA GAC GCT GAT GGT GGA GGA AGG GCC GTC TAT	48
Met Arg Gly Thr Pro Gly Asp Ala Asp Gly Gly Gly Arg Ala Val Tyr	
1 5 10 15	
CAA TCA ATG TGT AAA CCT ATT ACT GGG ACT ATT AAT GAT TTG AAT CAG	96
Gln Ser Met Cys Lys Pro Ile Thr Gly Thr Ile Asn Asp Leu Asn Gln	
20 25 30	
CAA GTG TGG ACC CTT CAG GGT CAG AAC CTT GTG GCA GTT CCA CGA AGG	144
Gln Val Trp Thr Leu Gln Gly Gln Asn Leu Val Ala Val Pro Arg Arg	
35 40 45	
ACC AGT GTG ACC CCA GTC ACT GTT GCT GTT ATC ACA TGC AAG TAT CCA	192
Thr Ser Val Thr Pro Val Thr Val Ala Val Ile Thr Cys Lys Tyr Pro	
50 55 60	
GAG GCT CTT GAG CAA GGC AGA GGG GAT CCC ATT TAT TTG GGA ATC CAG	240
Glu Ala Leu Glu Gln Gly Arg Gly Asp Pro Ile Tyr Leu Gly Ile Gln	
65 70 75 80	
AAT CCA GAA ATG TGT TTG TAT TGT GAG AAG GTT GGA GAA CAG CCC ACA	288
Asn Pro Glu Met Cys Leu Tyr Cys Glu Lys Val Gly Glu Gln Pro Thr	
85 90 95	
TTG CAG CTA AAA GAG CAG AAG ATC ATG GAT CTG TAT GGC CAA CCC GAG	336
Leu Gln Leu Lys Glu Gln Lys Ile Met Asp Leu Tyr Gly Gln Pro Glu	
100 105 110	
CCC GTG AAA CCC TTC CTT TTC TAC CGT GCC AAG ACT GGT AGG ACC TCC	384
Pro Val Lys Pro Phe Leu Phe Tyr Arg Ala Lys Thr Gly Arg Thr Ser	
115 120 125	
ACC CTT GAG TCT GTG GCC TTC CCG GAC TGG TTC ATT GCC TCC TCC AAG	432
Thr Leu Glu Ser Val Ala Phe Pro Asp Trp Phe Ile Ala Ser Ser Lys	
130 135 140	
GGA GAC CAG CCC ATC ATT CTG ACT TCA GAA CTT TGG CAG TCA TAC AAC	480
Gly Asp Gln Pro Ile Ile Leu Thr Ser Glu Leu Trp Gln Ser Tyr Asn	
145 150 155 160	

10920-04502260

ACT GCC TTT GAA TTA AAT ATT AAT G  
Thr Ala Phe Glu Leu Asn Ile Asn  
165

505

5

## (2) INFORMATION FOR SEQ ID NO:13:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

15

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Arg Gly Thr Pro Gly Asp Ala Asp Gly Gly Gly Arg Ala Val Tyr  
1 5 10 15  
Gln Ser Met Cys Lys Pro Ile Thr Gly Thr Ile Asn Asp Leu Asn Gln  
20 25 30  
Gln Val Trp Thr Leu Gln Gly Gln Asn Leu Val Ala Val Pro Arg Arg  
25 35 40 45  
Thr Ser Val Thr Pro Val Thr Val Ala Val Ile Thr Cys Lys Tyr Pro  
50 55 60  
Glu Ala Leu Glu Gln Gly Arg Gly Asp Pro Ile Tyr Leu Gly Ile Gln  
30 65 70 75 80  
Asn Pro Glu Met Cys Leu Tyr Cys Glu Lys Val Gly Glu Gln Pro Thr  
35 85 90 95  
Leu Gln Leu Lys Glu Gln Lys Ile Met Asp Leu Tyr Gly Gln Pro Glu  
100 105 110  
Pro Val Lys Pro Phe Leu Phe Tyr Arg Ala Lys Thr Gly Arg Thr Ser  
40 115 120 125  
Thr Leu Glu Ser Val Ala Phe Pro Asp Trp Phe Ile Ala Ser Ser Lys  
130 135 140  
Gly Asp Gln Pro Ile Ile Leu Thr Ser Glu Leu Trp Gln Ser Tyr Asn  
45 145 150 155 160  
Thr Ala Phe Glu Leu Asn Ile Asn  
165

50

## (2) INFORMATION FOR SEQ ID NO:14:

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## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

60

## (ii) MOLECULE TYPE: cDNA

(B) LOCATION: 67..573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

10	CCACGATTCA GTCCCCCTGGA CTGTAGATAA AGACCCCTTTC TTGCCAGGTG CTGAGACAAC	60
	CACACT ATG AGA GGC ACT CCA GGA GAC GCT GAT GGT GGA GGA AGG GCC Met Arg Gly Thr Pro Gly Asp Ala Asp Gly Gly Gly Arg Ala 1 5 10	108
15	GTC TAT CAA TCA ATG TGT AAA CCT ATT ACT GGG ACT ATT AAT GAT TTG Val Tyr Gln Ser Met Cys Lys Pro Ile Thr Gly Thr Ile Asn Asp Leu 15 20 25 30	156
20	AAT CAG CAA GTG TGG ACC CTT CAG GGT CAG AAC CTT GTG GCA GTT CCA Asn Gln Gln Val Trp Thr Leu Gln Gly Gln Asn Leu Val Ala Val Pro 35 40 45	204
25	CGA AGT GAC AGT GTG ACC CCA GTC ACT GTT GCT GTT ATC ACA TGC AAG Arg Ser Asp Ser Val Thr Pro Val Thr Val Ala Val Ile Thr Cys Lys 50 55 60	252
30	TAT CCA GAG GCT CTT GAG CAA GGC AGA GGG GAT CCC ATT TAT TTG GGA Tyr Pro Glu Ala Leu Glu Gln Gly Arg Gly Asp Pro Ile Tyr Leu Gly 65 70 75	300
35	ATC CAG AAT CCA GAA ATG TGT TTG TAT TGT GAG AAG GTT GGA GAA CAG Ile Gln Asn Pro Glu Met Cys Leu Tyr Cys Glu Lys Val Gly Glu Gln 80 85 90	348
40	CCC ACA TTG CAG CTA AAA GAG CAG AAG ATC ATG GAT CTG TAT GGC CAA Pro Thr Leu Gln Leu Lys Glu Gln Lys Ile Met Asp Leu Tyr Gly Gln 95 100 105 110	396
45	CCC GAG CCC GTG AAA CCC TTC CTT TTC TAC CGT GCC AAG ACT GGT AGG Pro Glu Pro Val Lys Pro Phe Leu Phe Tyr Arg Ala Lys Thr Gly Arg 115 120 125	444
50	ACC TCC ACC CTT GAG TCT GTG GCC TTC CCG GAC TGG TTC ATT GCC TCC Thr Ser Thr Leu Glu Ser Val Ala Phe Pro Asp Trp Phe Ile Ala Ser 130 135 140	492
55	TCC AAG AGA GAC CAG CCC ATC ATT CTG ACT TCA GAA CTT GGG AAG TCA Ser Lys Arg Asp Gln Pro Ile Ile Leu Thr Ser Glu Leu Gly Lys Ser 145 150 155	540
60	TAC AAC ACT GCC TTT GAA TTA AAT ATA AAT GAC TGA ACT CAGC CTAGAGGTGG Tyr Asn Thr Ala Phe Glu Leu Asn Ile Asn Asp 160 165	593
65	CAGCTTGGTC TTTGTCTTAA AGTTTCTGGT TCCCAATGTG TTTTCGTCTA CATTTTCTTA	653
70	GTGTCATTTT CACGCTGGTG CTGAGACAGG GGCAAGGCTG CTGTTATCAT CTCATTTTAT	713
75	AATGAAGAAG AAGCAATTAC TTCATAGCAA CTGAAGAACA GGATGTGGCC TCAGAAGCAG	773

GAGAGCTGGG TGGTATAAGG CTGTCCTCTC AAGCTGGTGC TGTGTAGGCC ACAAGGCATC 833  
 TGCATGAGTG ACTTTAAGAC TCAAAGACCA AACACTGAGC TTTCTTCTAG GGGTGGGTAT 893  
 5 GAAGATGCTT CAGAGCTCAT GCGCGTTACC CACGATGGCA TGA CTAGCAC AGAGCTGATC 953  
 TCTGTTTCTG TTTTGCTTTA TTCCCTCTTG GGATGATATC ATCCAGTCTT TATATGTTGC 1013  
 CAATATACCT CATTGTGTGT AATAGAACCT TCTTAGCATT AAGACCTTGT AAACAAAAAT 1073  
 10 AATTCTTGTG TTAAGTTAAA TCATTTTTGT CCTAATTGTA ATGTGTAATC TTAAAGTTAA 1133  
 ATAAACTTTG TGTATTTATA TAATAATAAA GCTAAACTG ATATAAAAAA AAAAAAAAAA 1193  
 15 AA 1195

## (2) INFORMATION FOR SEQ ID NO:15:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 169 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 25 (ii) MOLECULE TYPE: protein  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:  
 30 Met Arg Gly Thr Pro Gly Asp Ala Asp Gly Gly Gly Arg Ala Val Tyr  
 1 5 10 15  
 Gln Ser Met Cys Lys Pro Ile Thr Gly Thr Ile Asn Asp Leu Asn Gln  
 20 25 30  
 35 Gln Val Trp Thr Leu Gln Gly Gln Asn Leu Val Ala Val Pro Arg Ser  
 35 40 45  
 Asp Ser Val Thr Pro Val Thr Val Ala Val Ile Thr Cys Lys Tyr Pro  
 50 55 60  
 40 Glu Ala Leu Glu Gln Gly Arg Gly Asp Pro Ile Tyr Leu Gly Ile Gln  
 65 70 75 80  
 45 Asn Pro Glu Met Cys Leu Tyr Cys Glu Lys Val Gly Glu Gln Pro Thr  
 85 90 95  
 Leu Gln Leu Lys Glu Gln Lys Ile Met Asp Leu Tyr Gly Gln Pro Glu  
 100 105 110  
 50 Pro Val Lys Pro Phe Leu Phe Tyr Arg Ala Lys Thr Gly Arg Thr Ser  
 115 120 125  
 Thr Leu Glu Ser Val Ala Phe Pro Asp Trp Phe Ile Ala Ser Ser Lys  
 130 135 140  
 55 Arg Asp Gln Pro Ile Ile Leu Thr Ser Glu Leu Gly Lys Ser Tyr Asn  
 145 150 155 160  
 60 Thr Ala Phe Glu Leu Asn Ile Asn Asp 165

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